



SEQUENCE LISTING

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JUL 3 2002

TECH CENTER 1600/2900

<110> Willson, Tracy
Nicola, Nicos A.
Hilton, Douglas J.
Metcalf, Donald
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> Davies Collison Cave

<140> 09/688,286
<141> 2000-10-13

<150> 09/051,843
<151> 1998-06-29

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<170> PatentIn Ver. 2.0

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of mNR4

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region

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Met	Ala	Arg	Pro	Ala	Leu	Leu	Gly	Glu	Leu	Leu	Val	Leu	Leu	Leu	Trp	
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acc	gcc	acc	gtg	nnn	ggc	caa	gtt	gcc	gcg	gcc	aca	gaa	gtt	cag	cca	156
Thr	Ala	Thr	Val	Xaa	Gly	Gln	Val	Ala	Ala	Ala	Thr	Glu	Val	Gln	Pro	
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cct	gtg	acg	aat	ttg	agc	gtc	tct	gtc	gaa	aat	ctc	tgc	acg	ata	ata	204
Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Ile	Ile	
		35				40					45					

tgg	acg	tgg	agt	cct	cct	gaa	gga	gcc	agt	cca	aat	tgc	act	ctc	aga	252
Trp	Thr	Trp	Ser	Pro	Pro	Glu	Gly	Ala	Ser	Pro	Asn	Cys	Thr	Leu	Arg	
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Tyr	Phe	Ser	His	Phe	Asp	Asp	Gln	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	
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act	cat	cgt	aaa	gag	gaa	tta	ccc	ctg	gat	gag	aaa	atc	tgt	ctg	cag	348
Thr	His	Arg	Lys	Glu	Glu	Leu	Pro	Leu	Asp	Glu	Lys	Ile	Cys	Leu	Gln	
			85						90					95		
gtg	ggc	tct	cag	tgt	agt	gcc	aat	gaa	agt	gag	aag	cct	agc	cct	ttg	396
Val	Gly	Ser	Gln	Cys	Ser	Ala	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Pro	Leu	
			100					105					110			
gtg	aaa	aag	tgc	atc	tca	ccc	cct	gaa	ggc	gat	cct	gag	tcc	gct	gtg	444
Val	Lys	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	
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Thr	Glu	Leu	Lys	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	
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Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	His	Tyr	Thr	Leu	Tyr	
145					150					155					160	
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Tyr	Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	
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Arg	Glu	Gly	Gln	His	Ile	Ala	Cys	Ser	Phe	Lys	Leu	Thr	Lys	Val	Glu	
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cct	nnn	agt	ttt	gaa	cat	cag	aac	gtt	caa	ata	atg	gtc	aag	gat	aat	684
Pro	Xaa	Ser	Phe	Glu	His	Gln	Asn	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	
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gct	ggg	aaa	att	agg	cca	tcc	tgc	aaa	ata	gtg	tct	tta	act	tcc	tat	732
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Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	
225					230					235					240	
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Ala	Leu	Leu	Val	Gln	Trp	Lys	Asn	Pro	Gln	Asn	Phe	Arg	Ser	Arg	Cys	
			245					250						255		
tta	act	tat	gaa	gtg	gag	gtc	aat	aat	act	caa	acc	gac	cga	cat	aat	876
Leu	Thr	Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	
			260					265					270			

att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga	924
Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg	
275 280 285	
aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac	972
Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp	
290 295 300	
gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt	1020
Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe	
305 310 315 320	
gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt	1068
Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly	
325 330 335	
aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca	1116
Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro	
340 345 350	
gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg	1164
Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg	
355 360 365	
ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt	1212
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe	
370 375 380	
aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag	1260
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys	
385 390 395 400	
tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg	1308
Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val	
405 410 415	
ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc	1358
Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro	
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of mNR4

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<223> authors are unsure about the sequence assignment

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<223> authors are unsure about the sequence assignment

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20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
100 105 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
145 150 155 160

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
 420 425

<210> 3
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 alpha-chain

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 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15
 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 20 25 30
 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 35 40 45
 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60
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 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80
 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
 85 90 95
 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
 100 105 110

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Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	
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gat	tcc	agt	ttt	gaa	caa	cac	agt	gtc	caa	ata	atg	gtc	aag	gat	aat	684
Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	
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gca	gga	aaa	att	aaa	cca	tcc	ttc	aat	ata	gtg	cct	tta	act	tcc	cgt	732
Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg	
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gtg	aaa	cct	gat	cct	cca	cat	att	aaa	aac	ctc	tcc	ttc	cac	aat	gat	780
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225					230					235					240	
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Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	Cys	
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cta	ttt	tat	gaa	gta	gaa	gtc	aat	aac	agc	caa	act	gag	aca	cat	aat	876
Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn	
			260					265					270			
gtt	ttc	tac	gtc	caa	gag	gct	aaa	tgt	gag	aat	cca	gaa	ttt	gag	aga	924
Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg	
		275					280					285				
aat	gtg	gag	aat	aca	tct	tgt	ttc	atg	gtc	cct	ggg	gtt	ctt	cct	gat	972
Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	
	290					295					300					

act	ttg	aac	aca	gtc	aga	ata	aga	gtc	aaa	aca	aat	aag	tta	tgc	tat	1020
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Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Ser	Ile	Gly	
				325					330						335	
aag	aag	cgc	aat	tcc	aca	ctc	tac	ata	acc	atg	tta	ctc	att	gtt	cca	1116
Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val	Pro	
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gtc	atc	gtc	gca	ggg	gca	atc	ata	gta	ctc	ctg	ctt	tac	cta	aaa	agg	1164
Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	
			355					360						365		
ctc	aag	att	att	ata	ttc	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
			370				375					380				
aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	act	ctg	cac	tgg	aag	aag	1260
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys	
385					390					395					400	
tac	gac	atc	tat	gag	aag	caa	acc	aag	gag	gaa	acc	gac	tct	gta	gtg	1308
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
				405					410						415	
ctg	ata	gaa	aac	ctg	aag	aaa	gcc	tct	cag	tgatggagat	aattttatttt					1358
Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln							
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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Human IL-13 receptor
alpha-chain

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Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	Ile	35	40	45	
Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	Trp	50	55	60	
Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	65	70	75	80
Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln	85	90	95	
Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu	100	105	110	
Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	115	120	125	
Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	130	135	140	
Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	145	150	155	160
Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe	165	170	175	
Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys	180	185	190	
Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	195	200	205	
Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg	210	215	220	
Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn	Asp	225	230	235	240
Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	Cys	245	250	255	

Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn	
			260					265					270			
Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg	
		275					280					285				
Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	
	290					295					300					
Thr	Leu	Asn	Thr	Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Tyr	
305					310					315					320	
Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Ser	Ile	Gly	
				325					330					335		
Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val	Pro	
			340					345					350			
Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	
		355					360					365				
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
	370					375					380					
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys	
385					390					395					400	
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
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Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln							
			420					425								

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<211> 30

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:signal sequence of murine IL-3

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1				5				10					15			

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
20 25 30

<210> 6
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:N-terminal FLAG epitope-tag

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Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 7
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence:Oligo 1478 5'

<400> 7
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<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligo 1480 5'

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aactccacct tctacaccac ctgatctaga 30

<210> 9

<211> 5
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<223> Description of Unknown Organism:NR4 Motif

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<222> (3)
<223> Xaa may be any amino acid

<400> 9
Trp Ser Xaa Trp Ser
1 5

<210> 10
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<220>
<223> Description of Unknown Organism:N-term amino acid sequence
of mNR4 (major)

<220>
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<222> (24)
<223> Xaa may be any amino acid

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Asp Tyr Lys Asp Asp Asp Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25

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mNR4 (minor)

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<221> Unsure

<222> (24)

<223> Xaa may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25